

Refine Search

Search Results -

Term	Documents
KERATINOCYTE	2515
KERATINOCYTES	5020
GROWTH	279639
GROWTHS	4512
FACTOR	463022
FACTORS	431021
"2"	3748698
2S	13857
(KERATINOCYTE ADJ GROWTH ADJ FACTOR ADJ "2").USPT.	18
(KERATINOCYTE GROWTH FACTOR 2).USPT.	18

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L1

Search History

 DATE: Tuesday, July 18, 2006 [Printable Copy](#) [Create Case](#)
Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=ADJ

L1 keratinocyte growth factor 2 18 L1

END OF SEARCH HISTORY

SCORE Table of Contents for Application 10733311

[Score Home
Page](#)[Retrieve Application
List](#)[SCORE System
Overview](#)[SCORE
FAQ](#)[Comments /
Suggestions](#)

This page gives information regarding the number of sequences, mega tables, and other mega items associated with the requested application.

Summary of Information

7/18/06

Number of Sequences	176
Number of Megatables	0
Number of SearchResults	6
Number of Computer Program Listings	0
Number of Other Mega Items	0

Detailed Sequence Information

[View a version list for this application](#)

This Sequence Listing comprises **176** SEQ ID Nos. To view one or more of these sequences, indicate the numeric SEQ ID or range of numeric SEQ IDs in the text box below.

To obtain the header information submitted with a Sequence Listing, please submit a request for SEQ ID NO: 1.

Enter individual SEQ ID Nos (1,3,7,9) or Range (1-10) or a combination of individual and range (1, 3-8).

Download All Sequences:

Comments /
Suggestions

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1125	100.0	627	2	BD022747	BD022747 Utilizati
5	1125	100.0	627	2	BD136525	BD136525 Therapeut
6	1125	100.0	627	2	BD228651	BD228651 Regulatio
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13	1125	100.0	627	2	DD179080	DD179080 Albumin F
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ALIGNMENTS

RESULT 1

AR099137

LOCUS AR099137 627 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6077692.

ACCESSION AR099137

VERSION AR099137.1 GI:12808903

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 627)

AUTHORS Ruben,S.M., Jimenez,P., Duan,D.Roxanne., Rampy,M.A., Mendrick,D., Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J. and Gentz,R.L.

TITLE Keratinocyte growth factor-2

JOURNAL Patent: US 6077692-A 1 20-JUN-2000;

FEATURES Location/Qualifiers

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US-10-733-311-2 (1-208) x AR099137 (1-627)

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SCORE Search Results Details for Application 10733311 and Search Result us-10-733-311-2.p2n.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10733311 and Search Result us-10-733-311-2.p2n.rnpbm.

[start](#)

[Go Back to previous](#)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2006, 00:18:08 ; Search time 1427 Seconds
(without alignments)
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Delop 6.0 , Delext 7.0

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1125	100.0	627	3	US-09-853-666-1	Sequence 1, Appli
2	1125	100.0	627	3	US-09-345-373-1	Sequence 1, Appli
3	1125	100.0	627	7	US-10-194-443-1	Sequence 1, Appli
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6	1125	100.0	627	7	US-10-035-212-1	Sequence 1, Appli
7	1125	100.0	627	7	US-10-131-985-12	Sequence 12, Appl
8	1125	100.0	627	8	US-10-665-526-1	Sequence 1, Appli
9	1125	100.0	627	8	US-10-695-957-1	Sequence 1, Appli
10	1125	100.0	627	8	US-10-302-812-35	Sequence 35, Appl
11	1125	100.0	627	8	US-10-322-696-47	Sequence 47, Appl
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13	1125	100.0	627	8	US-10-384-339C-55	Sequence 55, Appl
14	1125	100.0	627	9	US-10-733-311-1	Sequence 1, Appli
15	1125	100.0	627	9	US-10-901-417-12	Sequence 12, Appl
16	1125	100.0	627	9	US-10-901-210-1	Sequence 1, Appli
17	1125	100.0	627	10	US-10-756-149-2519	Sequence 2519, Ap
18	1125	100.0	627	10	US-10-775-204-36	Sequence 36, Appl
19	1125	100.0	627	10	US-10-775-204-37	Sequence 37, Appl
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21	1125	100.0	627	10	US-10-775-204-66	Sequence 66, Appl
22	1125	100.0	627	10	US-10-775-204-213	Sequence 213, App
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ALIGNMENTS

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US-09-853-666-1

: Sequence 1, Application US/09853666

; Patent No. US20020016295A1

; GENERAL INFORMATION:

: APPLICANT: Gentz, Reiner L.

: APPLICANT: Chopra, Arvind

APPLICANT: Kaushal, Parveen

; APPLICANT: Spitznagel, Thomas

; APPLICANT: Unsworth, Edward

; APPLICANT: Khan, Fazal

; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations

; FILE REFERENCE: 1488.1030001

; CURRENT APPLICATION NUMBER: US/09/853,666

: CURRENT FILING DATE: 2001-05-14

: PRIOR APPLICATION NUMBER: 09/218,444

: PRIOR FILING DATE: 1998-12-22

; NUMBER OF SEO ID NOS: 33

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; SOFTWARE: PatentIn Ver. 2.0

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; SEO ID NO 1

; LENGTH: 627

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE :

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; NAME/KEY: CDS

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; LOCATION: (1) .. (624)

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US-09-853-666-1

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Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match:	100.0%	Indels:	0
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US-10-733-311-2 (1-208) x US-09-853-666-1 (1-627)

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SCORE Search Results Details for Application 10733311 and Search Result us-10-733-311-2.p2n.rnpbn.

[Score Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE
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Comments /
Suggestions

This page gives you Search Results detail for the Application 10733311 and Search Result us-10-733-311-2.p2n.rnpbn.

start

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	447	39.7	463	7	US-11-005-836-14	Sequence 14, Appl
6	446	39.6	521	7	US-11-005-836-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1

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; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
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; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
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SCORE Search Results Details for Application 10733311 and Search Result us-10-733-311-2.p2n.rnpm.

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start

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OM protein - nucleic search, using frame plus p2n model

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SUMMARIES

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start

[Go Back to previous page](#)

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OM protein - nucleic search, using frame_plus_p2n model

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27	1125	100.0	627	7	US-11-429-276-36	Sequence 36, Appl
28	1125	100.0	627	7	US-11-429-276-37	Sequence 37, Appl
29	1125	100.0	627	7	US-11-429-276-65	Sequence 65, Appl
30	1125	100.0	627	7	US-11-429-276-66	Sequence 66, Appl
31	1125	100.0	627	7	US-11-429-276-213	Sequence 213, App
32	1125	100.0	627	7	US-11-429-276-214	Sequence 214, App
33	1125	100.0	627	7	US-11-429-276-1348	Sequence 1348, Ap
34	1125	100.0	627	7	US-11-429-276-1349	Sequence 1349, Ap
35	1125	100.0	627	7	US-11-429-276-1352	Sequence 1352, Ap
36	1125	100.0	627	7	US-11-429-276-1356	Sequence 1356, Ap
37	1125	100.0	627	7	US-11-429-276-1357	Sequence 1357, Ap
38	1125	100.0	627	7	US-11-429-276-1358	Sequence 1358, Ap
39	1125	100.0	627	7	US-11-429-276-1362	Sequence 1362, Ap
40	1125	100.0	627	7	US-11-433-832-44639	Sequence 44639, A
41	1125	100.0	1319	6	US-10-669-920-1206	Sequence 1206, Ap
42	1121	99.6	627	7	US-11-479-419-2	Sequence 2, Appli
43	1121	99.6	2654	7	US-11-433-832-834	Sequence 834, App

SCORE Search Results Details for Application 10733311 and Search Result us-10-733-311-2.p2n.rst.

[Score Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE
FAO

Comments /
Suggestions

This page gives you Search Results detail for the Application 10733311 and Search Result us-10-733-311-2.p2n.rst.

start

[Go Back to previous page](#)

GenCore version 5.1.9
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OM protein - nucleic search, using frame plus p2n model

```
Run on:      July 13, 2006, 23:10:15 ; Search time 4436 Seconds
              (without alignments)
              3933.010 Million cell updates/sec
```

Title: US-10-733-311-2
Perfect score: 1125
Sequence: 1 MWKWILTHCASAFPHLPGCC.....GQKTRRKNTSAHFLPMVVHS 208

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop 6.0 , Delext 7.0
```

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10733311/runat_13072006_102736_21805/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10733311_CGN_1_1_9528_runat_13072006_102736_21805 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      EST:*
           1:   qb est1:*
```

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1125	100.0	627	14	AY404415	AY404415 Homo sapi	
2	1075	95.6	627	14	AY404416	AY404416 Pan trogl	
3	1045.5	92.9	630	14	AY404417	AY404417 Mus muscu	
4	1045.5	92.9	1462	6	AK034742	AK034742 Mus muscu	
5	1045.5	92.9	1912	6	AK085244	AK085244 Mus muscu	
6	1045.5	92.9	3169	6	AK045267	AK045267 Mus muscu	
7	1045.5	92.9	3435	6	AK141633	AK141633 Mus muscu	
8	987.5	87.8	659	7	BB660592	BB660592 BB660592	
9	986	87.6	660	9	DR003252	DR003252 TC110895	
10	948.5	84.3	588	4	BY729848	BY729848 BY729848	
11	928	82.5	679	4	BY724159	BY724159 BY724159	
12	904	80.4	510	9	DA804788	DA804788 DA804788	
c 13	875.5	77.8	531	2	BG066324	BG066324 H3041F04-	
14	855.5	76.0	924	3	BU148680	BU148680 AGENCOURT	
15	825	73.3	470	4	BX280011	BX280011 BX280011	
16	798	70.9	693	2	BF983177	BF983177 602309088	
17	684	60.8	437	7	BB848710	BB848710 BB848710	
18	641.5	57.0	631	9	DN127342	DN127342 1141335 M	
c 19	641.5	57.0	631	9	DN127696	DN127696 1141719 M	
20	616.5	54.8	633	7	BB626844	BB626844 BB626844	
21	592	52.6	562	3	BP380072	BP380072 BP380072	
22	554	49.2	773	10	DR430894	DR430894 nax36d04.	
23	549	48.8	855	14	CT400167	CT400167 Sus scrof	
24	537	47.7	558	4	BX471703	BX471703 DKFZp686A	
25	524.5	46.6	825	9	DN819500	DN819500 UMC-bconb	
26	514	45.7	520	9	DB177119	DB177119 DB177119	
c 27	505	44.9	742	2	BJ896070	BJ896070 BJ896070	
28	493	43.8	651	7	BB660297	BB660297 BB660297	
29	485.5	43.2	422	4	CB763535	CB763535 AMGNNUC:N	
30	481.5	42.8	1821	6	AK037172	AK037172 Mus muscu	
c 31	478.5	42.5	739	3	BQ191883	BQ191883 UI-R-DR1-	
32	474.5	42.2	581	3	BP207143	BP207143 BP207143	
33	474.5	42.2	830	3	BU748617	BU748617 CH3#021_C	
c 34	473.5	42.1	907	4	BX372151	BX372151 BX372151	
35	473.5	42.1	1556	6	CR593889	CR593889 full-leng	
36	473.5	42.1	1597	6	CR858873	CR858873 Pongo pyg	
37	473.5	42.1	1694	6	CR617541	CR617541 full-leng	
38	473.5	42.1	1909	6	CR609737	CR609737 full-leng	

39	472.5	42.0	1132	1	AL554670	AL554670	AL554670
40	468.5	41.6	2288	6	AK033934	AK033934	Mus muscu
41	465.5	41.4	2623	6	AK086639	AK086639	Mus muscu
42	451	40.1	709	4	BX094084	BX094084	BX094084
43	443.5	39.4	1166	8	CN642510	CN642510	ILLUMIGEN
44	437	38.8	992	4	BY708810	BY708810	BY708810
45	437	38.8	2126	6	AK008922	AK008922	Mus muscu

ALIGNMENTS

RESULT 1

AY404415

LOCUS AY404415 627 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens FGF10 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404415

VERSION AY404415.1 GI:39760392

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 627)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 627)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source

1..627

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

gene

<1..>627

/gene="FGF10"

/locus_tag="HCM1883"

ORIGIN

Alignment Scores:

Pred. No.:	1.48e-109	Length:	627
Score:	1125.00	Matches:	208
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	14	Gaps:	0

Day : Tuesday
Date: 7/18/2006

Time: 07:28:35

 **PALM INTRANET**

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Back to [PALM](#) | [ASSIGNMENT](#) | [OASIS](#) | [Home page](#)